

**Poster 9. Development and characterization of wheat–alien translocation lines conferring stem rust resistance from *Aegilops searsii* and *Ae. geniculata*.**

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Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is potentially one of the most damaging wheat diseases. Although crop loss to stem rust has been infrequent in the past several decades, the emergence of the Ug99 lineage of stem rust races now threatens a large proportion of the wheat acres in the world. Exploiting novel genes effective against Ug99 from wild relatives of wheat is one of the most promising strategies for the protection of wheat production. In this study, resistance to Ug99 was identified on the short arm of 3S<sup>s</sup> of *Ae. searsii* (2n=2x=14, S<sup>s</sup>S<sup>s</sup>) and long arm of 5M<sup>s</sup> of *Ae. geniculata* (2n=2x=28, U<sup>s</sup>M<sup>s</sup>) by testing of a disomic and ditelosomic addition lines with the chromosomes. To transfer the gene(s) into common wheat, we produced three double-monosomic chromosome populations (3A/3S<sup>s</sup>, 3B/3S<sup>s</sup>, and 3D/3S<sup>s</sup>) of wheat–*Ae. searsii* and two populations of T550 (T5M<sup>s</sup>S·5M<sup>s</sup>L–5DL) crossed with *ph1b* mutant and Lakin, and then applied integrated molecular and cytogenetic approaches to develop wheat–alien recombinants conferring stem resistance. Three wheat–*Ae. searsii* compensating, Robertsonian translocations (T3S<sup>s</sup>S·3AL, T3S<sup>s</sup>S·3BL and T3S<sup>s</sup>S·3DL) and three wheat–*Ae. geniculata* translocation lines with shortened 5M<sup>s</sup>L were selected and confirmed on the basis of genomic in situ hybridization and analysis of 3S<sup>s</sup>S and 5M<sup>s</sup> using homoologous wheat chromosome-specific SSR/STS–PCR markers. These translocation lines were highly or moderately resistant to stem rust race RKQQ. Evaluation of Ug99 resistance and agronomic characterization of the recombinants are currently in progress; efforts to reduce potential linkage drag associated with 3S<sup>s</sup>S of *Ae. searsii* also is underway.

**Poster 10. Reactive oxygen species are involved in plant defense against a gall midge.**

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Reactive oxygen species (ROS) play a major role in plant defense against pathogens, but evidence for their role in defense against insects is still preliminary and inconsistent. In this study, we examined the potential role of ROS in defense of wheat and rice against Hessian fly (*Mayetiola destructor*) larvae. Rapid and prolonged accumulation of H<sub>2</sub>O<sub>2</sub> was detected in wheat plants at the attack site during incompatible interactions. Increased accumulation of both H<sub>2</sub>O<sub>2</sub> and superoxide was detected in rice plants during nonhost interactions with the larvae. No increase in accumulation of either H<sub>2</sub>O<sub>2</sub> or superoxide was observed in wheat plants during compatible interactions. A global analysis revealed changes in the abundances of 250 wheat transcripts and 320 rice transcripts encoding proteins potentially involved in ROS homeostasis. A large number of transcripts encoded class-III peroxidases that increased in abundance during both incompatible and nonhost interactions, whereas the levels of these transcripts decreased in susceptible wheat during compatible interactions. The higher levels of class-III peroxidase transcripts were associated with elevated enzymatic activity of peroxidases at the attack site in plants during incompatible and nonhost interactions. Overall, our data indicate that class-III peroxidases may play a role in ROS generation in resistant wheat and nonhost rice plants during response to Hessian fly attacks.